Dr. Johannsen
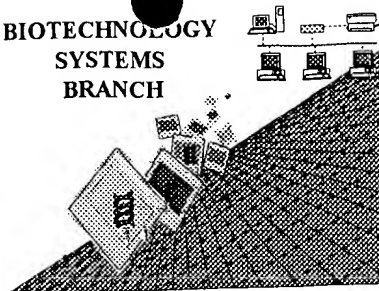
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _O9/581,500_

Source: _1655_

Date Processed by STIC: _1/24/2001_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED CORRECTION   SERIAL NUMBER: _09/581,500_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics — The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos — The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length — The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering — The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII — This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES) — Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES) — Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES) — Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES) — Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

1655

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/581,500

DATE: 01/24/2001
TIME: 13:18:27

Input Set : A:\B01927019.txt
Output Set: N:\CRF3\01242001\I581500.raw

**Does Not Comply
Corrected Diskette Needed**

```
    3  <110> APPLICANT: Van Broeckhoven, Christine
    4         Raeymaekers, Peter
    5         Del-Favero, Jurgen
    7  <120> TITLE OF INVENTION: MOOD DISORDER GENE
    9  <130> FILE REFERENCE: B0192/7019
   11  <140> CURRENT APPLICATION NUMBER: US/09/581,500
   12  <141> CURRENT FILING DATE: 2000-11-14
   14  <150> PRIOR APPLICATION NUMBER: GB 9726804.9
   15  <151> PRIOR FILING DATE: 1997-12-18
   17  <150> PRIOR APPLICATION NUMBER: PCT/EP98/08543
   18  <151> PRIOR FILING DATE: 1998-12-17
   20  <160> NUMBER OF SEQ ID NOS: 23
   22  <170> SOFTWARE: PatentIn Ver. 2.0
```

ERRORED SEQUENCES

```
  145  <210> SEQ ID NO: 12
  146  <211> LENGTH: 656
  147  <212> TYPE: DNA
  148  <213> ORGANISM: Homo sapiens
  150  <400> SEQUENCE: 12
  151  gccaacaaac aaaatgaaat aagacctggg atgtattttt tggccaaggc aattagaaaa  60
  152  tgattagtat ccttatcagg agcaatttca gagaatgttt gggtggacgt ctaactacag  120
  153  tggagtcaaa cgtgaatcaa cggtgaaaaa aggacaatag ccaatgtgta cactttttat  180
  154  aaaaaccacc ctccaaggac caggcactgg ccctctctcc ggtgcccaca gacatccaca  240
  155  caggcccaaa gaatcaggga ttgcacaagc cagagcaatc gaacggttct gagtcatctg  300
  156  ccggaagcct tgccctcaat caaggcggac gtgaagcatc tacaaaggag gaatagtcaa  360
  157  agcagcagcg gcggcggcgg cggcggcagc agcagcagca gcaggaggtg ggggcctctg  420
  158  ccaggtaccg ggcggggcag gcacggaggt gcccaggttc ccgcggaggc cacctcttcc  480
  159  ctggagtgcg tgagagaggg gaagggagga aggccagagc aggaatcaga gcgaggcaaa  540
  160  ggcgggcagg aactaxgaga atgacsgcgg gaggcggccg ggaaagaaax tctcgggct   600
  161  gtgggggtdx ccctggcacc agccgggggtc ccaagccccca ccgcgagacc ccgcga       656
```

Per 1.822 of Sequence Rules, do not use "x" in the sequence itself. Use n and explain what n represents in <2207-<2237 section.

See next page for more errors.

```
<210> 3
<211> 154
<212> DNA
<213> Homo sapiens

<400> 3
acataaaatg tcgctcaaaa acaattatgt gtgtctacac atatgggaaa gcaggaaaca    60
aatttgttta caacatacat tacttttgtt ttttaggcaa gataaaatgt cctacctcca   120
aaaccaccag cacngtccgc aataactata catc                               154
```

see item 10 on Error Summary Sheet (global error)

FYI:

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

Input Set : A:\B01927019.txt
Output Set: N:\CRF3\01242001\I581500.raw

```
L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:51 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:51 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:51 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:51 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
L:51 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:52 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:3
L:52 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:52 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:52 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:3
M:340 Repeated in SeqNo=3
L:63 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:63 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:63 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:63 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:63 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:64 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:64 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:64 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:64 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
M:340 Repeated in SeqNo=4
L:73 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:73 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:73 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:73 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:73 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:74 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:74 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:74 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:74 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
M:340 Repeated in SeqNo=5
L:75 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:5
L:75 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:5
L:75 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:5
L:75 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:84 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:84 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:84 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:84 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:84 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:6
L:87 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:87 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
L:87 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:87 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
M:340 Repeated in SeqNo=6
L:88 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:88 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
```

Input Set : A:\B01927019.txt
Output Set: N:\CRF3\01242001\I581500.raw

```
L:88 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:6
L:88 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:96 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:7
L:96 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:7
L:96 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:7
L:96 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:96 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
L:108 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:108 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
L:108 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:8
L:108 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:8
L:108 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
L:109 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:8
L:109 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:8
M:340 Repeated in SeqNo=8
L:117 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
M:340 Repeated in SeqNo=9
L:128 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:10
M:340 Repeated in SeqNo=10
L:141 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:160 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2
L:161 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:218 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
M:340 Repeated in SeqNo=18
L:252 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:21
M:340 Repeated in SeqNo=21
```